



1/16

FIGURE 1A

CCTTTCCTCTGTCTGTAAAGATTCAACATTTTAAATCAGTTAAATACTTTGTCTCTCTCCATCAGAAAGTAAATACATAAGAA
30 M H Y F Q V L A A L S V F M I I A C L T R G K P L E N W K K
ATGCATTATTTGGAGTATTAGCTGCACCTGTCTGTTTCAATATCATTCCTGACAAGAGCGCAAGCCTTTGGAAACTGGAAAG
L P V M E E S D A F F H D P G E V E H D T H F D F K S F L E 60
CTACCAGTTATGGAAGAGTCTGATGCATTCTTTCATGATCCTGGGNAAGTGGAAACATGACACCCACTTTGACTTTTAAATCTTCTTGGAG
N M K T D L L R S L N L S R V P S Q V K T K E E P P Q F M I 90
AATATGAAGACAGATTACTAAGAAGTCTGMAATTTATCAAGGTCCCTCACAAAGTGAAGACCAAGAGAGCCACACAGTTCATGATT
D L Y N R Y T A D K S S I P A S N I V R S F S T E D V V S L 120
GATTATACAACAGATATACAGCGGACAAAGTCTCCATCCCTGCATCCCAACATCGTGAGGAGCTTCAGCACTGAAGATGTTGTTTCTTTA
I S P E E H S F Q K H I L L F N I S I P R Y E E V T R A E L 150
ATTTCAACAGAACACACTATTTCAGAAACACACATCTTGTCTCTCAACATCTCTATTCCACGATATGAGGNAAGTCAACAGAGCTGAACCTG
R I F I S C H K E V G S P S R L E G N M V I Y D V L D G D H 180
AGAATCTTTATCTCTGTCAAGGAAGTTGGTCTCCCTCCAGACTGGNAAGCAACATGGTCACTTTATGATGTTCTAGATGGAGACCAT
W E N K E S T K S L L V S H S I Q D C G W E M F E V S S A V 210
TGGGAAACAAGAAAGTACCAATCTTTACTTGTCTCTCACAGTATTACGAGACTGTGGCTGGAGATGTTTGAGGTGTCCAGCGCTGCG
K R W V K A D K M K T K N K L E V V I E S K D L S G F P C G 240
AAAGATGGGTCAAGGCAGACAGATGAAGACTAAACAAGCTAGAGGTTGTTATAGAGAGTAAGGATCTGAGTGGTTTCTTCTTGTGGG



2/16

FIGURE 1B

K L D I T V T H D T K N L P L L I V F S N D R S N G T K E T 270
AAGCTGGATATTACTGTACTCATGACACTAAATACTGCCCTATTATAGTGTCTCCAATGATCGCAGCAATGGACAAAGAGACC
K V E L R E M I V H E Q E S V L N K L G K N D S S E E E Q 300
AAAGTGGAGCTCCGGGAGATGATTGTTGATGAACAAGAAAGTGTGCTAAACAATAAGGAAGAACGACTCTTCATCTGGAAGAAGACAG
R E E K A I A R P R Q H S S R S K R S I G A N H C R R T S L 330
AGAGAAGAAAGCCATTGCTAGGCCCCGTCAGCATTCCTCCAGAACGAGAGCATAGGAGCAACCACTGTGCGAGAACGTCACCTC
H V N F K E I G W D S W I I A P K D Y E A F E C K G G C F F 360
CATGTGAACCTTTAAAGAAATAGGTGGGATTCTTGGATCATTCACCCAAAGATTATGAGGCTTTTGAGTGTAAAGGAGGTTGCTTCTTC
P L T D N V T P T K H A I V Q T L V H L Q N P K K A S K A C 390
CCCCACAGATAATGTTACGCCCAACCAACATGCTATTGTCCAGACTCTGGTGCACTCTCCAAACCCCAAGAAAGCTTCCAAAGGCCTGT
C V P T K L D A I S I L Y K D D A G V P T L I Y N Y E G M K 420
TGTTGCCAACTAAATTGGATGCAATCTCTATTCTTTATAAGGATGATGCTGTGCTGCCCACTTTGATATATACTATGAAGGGATGA
V A E C G C R 427
GTGGCAGAAATGTGGCTGCAGGTAGTATATGCTGAATATCTAAGAAATATACTCTTTTCTGCTGTGTGAACTGTACATTAGTGATGCAA
ATGAAATCCTTGCAACAAGGTTTGGAGCACGGCATGGGGCTGGTTGTTGCTGCTTTTAAAGGAAGATGGCATTAAAGAATGGC
AATCACTGTAAATACCTCGCATTATATACCATTAATTAAACTTTGTGAGATTGAAAAAATAAAAAA